



A service of the National Library of Medicine
and the National Institutes of Health

www.pubmed.gov

My NCBI

[Sign In] [Register]

All Databases

PubMed

Nucleotide

Protein

Genome

Structure

OMIM

PMC

Journals

Books

Search PubMed for site specific recombination, gram positive

Preview

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

About Entrez

Text Version

Entrez PubMed

Overview

Help | FAQ

Tutorials

New/Noteworthy

E-Utilities

PubMed Services

Journals Database

MeSH Database

Single Citation Matcher

Batch Citation Matcher

Clinical Queries

Special Queries

LinkOut

My NCBI

Related Resources

Order Documents

NLM Mobile

NLM Catalog

NLM Gateway

TOXNET

Consumer Health

Clinical Alerts

ClinicalTrials.gov

PubMed Central

- Search History will be lost after eight hours of inactivity.
- Search numbers may not be continuous; all searches are represented.
- To save search indefinitely, click query # and select Save in My NCBI.
- To combine searches use #search, e.g., #2 AND #3 or click query # for more options.

Search

Most Recent Queries

Time Result

#31	Search site specific recombination, gram positive	13:58:04	45
#30	Search site-specific recombination, gram positive	13:50:07	1629
#24	Search intramolecular recombination, gram positive	13:49:51	4
#11	Search beta recombinase	13:49:35	958
#29	Search b	13:49:26	684797
#23	Search intramolecular recombination activity, gram positive	13:25:07	0
#22	Search intramolecular recombination activity, beta recombinase	13:24:49	2
#21	Search intramolecular recombination activity	13:24:42	216
#12	Search beta recombinase, review	12:58:46	38
#10	Search Gene Therapy Inc	12:17:31	613
#8	Search Lechardeur	12:13:50	21
#7	Search galactosyl spermine	09:33:02	1
#6	Search galactosyl spermine	09:32:57	0
#5	Search mannosyl spermine	09:32:51	0
#4	Search lactosyl spermine	09:32:45	0
#2	Search cholesteryl spermine	09:31:03	7
#1	Search cholesteryl spermine, lactosyl spermine	09:30:49	0

Clear History

Write to the Help Desk

NCBI | NLM | NIH

Department of Health & Human Services

Privacy Statement | Freedom of Information Act | Disclaimer

Nov 6 2006 15:24:20

Appendix

Site-specific recombinase [*Streptococcus pyogenes*], plasmid pSM19035

Accession YP_232767.1 GI:63021996

makigyarvsskeqnldrlqlqgvskvfdsklsgqsverpqlqamlnyiregdivvvteldrlgrnnkeltelmnaiqqkgatlevlnlpsmngie
denlrrlinnlvielykyqaeserkrikerqaqgieiaksgkfkgrqhkfkendprlkhafdlflngcsdkeveeqtginrrtfrfryrtrynvtvdqrknk
gkrds

A partial list of sequences producing significant alignments	Score (Bits)	E Value
gi 63021985 ref YP_232754.1 site-specific recombinase [Strep...	316	3e-85
gi 81176607 gb ABB59535.1 putative resolvase [Pediococcus acidi	305	7e-82
gi 10956207 ref NP_044464.1 resolvase [Streptococcus agalact...	302	8e-81
gi 392559 gb AAA73395.1 resolvase protein [Streptococcus agalac	301	1e-80
gi 6690329 gb AAF24086.1 AF117258_3 resolvase [Staphylococcus au	297	2e-79
gi 3023049 gb AAC38605.1 resolvase [Enterococcus faecalis]	293	4e-78
gi 6746431 gb AAF27558.1 putative resolvase [Lactococcus lactis	254	1e-66
gi 6739586 gb AAF27319.1 putative resolvase [Lactococcus lactis	251	1e-65
gi 58701072 gb AAW81284.1 hypothetical protein [Lactobacillus p	236	3e-61
gi 108736165 gb ABG00294.1 ORF12 [Lactococcus lactis]	236	4e-61
gi 116334884 ref YP_796409.1 Site-specific recombinase, DNA ...	235	1e-60
gi 56707177 ref YP_163807.1 putative resolvase [Lactobacillu...	234	2e-60
gi 75181775 gb ABA12807.1 hypothetical protein [Lactobacillus p	233	3e-60
gi 75182232 gb ABA12841.1 conserved hypothetical protein [La...	233	4e-60
gi 5420101 emb CAB46556.1 putative resolvase [Streptococcus the	231	2e-59
gi 29377950 ref NP_817076.1 site-specific recombinase, resol...	216	5e-55
gi 69247432 ref ZP_00604345.1 recombinase Sin [Enterococcus ...	185	1e-45
gi 116326678 ref YP_796452.1 Site-specific recombinase, DNA ...	156	6e-37
gi 116490744 ref YP_810288.1 Site-specific recombinase, DNA ...	134	2e-30
gi 69247633 ref ZP_00604427.1 Resolvase, N-terminal:Resolvas...	133	4e-30
gi 69250457 ref ZP_00605155.1 Resolvase, N-terminal [Enteroc...	129	8e-29
gi 81330302 ref YP_398694.1 hypothetical protein pHTbeta_52 ...	127	4e-28
gi 116493435 ref YP_805170.1 Site-specific recombinase, DNA ...	119	7e-26
gi 37595767 ref NP_932185.1 Res2 [Staphylococcus aureus] >gi...	117	2e-25
gi 82743151 ref ZP_00905814.1 integrative genetic element Gs...	115	1e-24
gi 495089 gb AAA26675.1 recombinase >gi 8574415 emb CAB94806...	115	2e-24
gi 1086524 gb AAB08926.1 invertase-enterococcal	113	4e-24
gi 82751033 ref YP_416774.1 recombinase [Staphylococcus aure...	112	1e-23
gi 22476843 gb AAM97333.1 AF426833_2 recombinase Sin [Staphyloco	111	2e-23
gi 13793990 gb AAK38455.1 recombinase Sin [Staphylococcus epide	110	3e-23
gi 22476850 gb AAM97339.1 AF426834_5 recombinase Sin [Staphyloco	110	5e-23
gi 70727309 ref YP_254225.1 recombinase Sin [Staphylococcus ...	109	6e-23
gi 11230707 emb CAC16669.1 recombinase [Staphylococcus haemolyt	109	9e-23
gi 8980455 emb CAB96927.1 Bin3 protein [Stenotrophomonas maltop	108	2e-22
gi 38257108 ref NP_940770.1 recombinase [Staphylococcus warn...	107	3e-22
gi 116514884 ref YP_813790.1 Site-specific recombinase, DNA ...	107	5e-22
gi 111017138 ref YP_700110.1 possible resolvase, N-terminal ...	106	6e-22
gi 11968214 ref NP_072000.1 recombinase [Enterococcus faecal...	105	1e-21
gi 110628945 gb ABG79938.1 resolvase [Lactobacillus reuteri]	104	2e-21
gi 32455946 ref NP_862404.1 putative transposon resolvase [M...	104	3e-21

Application/Control Number: 10/808,161

Art Unit: 1633

Example Alignment

gi|116326678|ref|YP_796452.1| Site-specific recombinase, DNA invertase Pin related protein, [Lactobacillus casei ATCC 334]

gi|116106496|gb|ABJ71637.1| Site-specific recombinase, DNA invertase Pin related protein, [Lactobacillus casei ATCC 334]

Score = 156 bits (394), Expect = 6e-37, Method: Composition-based stats.

Identities = 88/156 (56%), Positives = 121/156 (77%), Gaps = 2/156 (1%)

```
Query 1 MAKIGYARVSSKEQNLDRLQALQ--GVSKVFSDKLSGQSVERPQLQAMLNYIREGDIVV 58
      M+KIGYARVS+++QNL RQ++ L GV+K+F +KLSG++ +RPQL+AML+YIR+ D VV
Sbjct 1 MSKIGYARVSTRDQNLARQIEQLHDAGVKNIFQEKLSGKNADRPQLKAMLDYIRDDDEVV 60

Query 59 VTELDRLGRNNKELTELMNAIQKKGATLEVLNLPMSGIEDENLRRLINNLVIELYKYQA 118
      V LDRLGRN+ +LT+++ I+ +GA L VLNLP IED NLR LI +++ELYKY A
Sbjct 61 VLSLDRLGRNSHDLTDIIETIRHRGAQLNVNLPSFASIEDPNLRNLITTIIVELYKYIA 120

Query 119 ESERKRIKERQAQGIEIAKSKGKFKGRQHFKENDP 154
      + ER+ IK RQ QGIEIAK +GK+KG+ ++ + P
Sbjct 121 QEERETIKIRQQQGIEIAKRQGYKKGKIREYGPHSP 156
```